SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
       (A) NAME: Peter Ruhdal Jensen
       (B) STREET: Soegaardsvej 19
       (C) CITY: Gentofte
       (E) COUNTRY: Denmark
       (F) POSTAL CODE (ZIP): DK-2820

    (ii) TITLE OF INVENTION: Artificial promoter libraries for selected
        organisms and promoters derived from such libraries

    (iii) NUMBER OF SEQUENCES: 58

    (iv) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

    (vi) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: DK 886/96
       (B) FILING DATE: 23-AUG-1996

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 100 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
       (A) NAME/KEY: promoter
       (B) LOCATION:26..82
       (C) IDENTIFICATION METHOD: experimental
       (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
         /standard_name= "Artificial promoter library"
         /note= "A degenerated sequence specifying a mixture of
         artificial promoters covering a wide range of expression
         in small steps in L. lactis"

    (ix) FEATURE:
       (A) NAME/KEY: misc_feature
       (B) LOCATION:31..45
       (D) OTHER INFORMATION:/standard_name= "Consensus
         sequence"

    (ix) FEATURE:
       (A) NAME/KEY: misc_feature

                    (B) LOCATION:60..69
                    (D) OTHER INFORMATION:/standard_name= "Consensus
                         sequence"

          (ix) FEATURE:
                    (A) NAME/KEY: misc_feature
                    (B) LOCATION:74..82
                    (D) OTHER INFORMATION:/standard_name= "Consensus
                         sequence"

          (ix) FEATURE:
                    (A) NAME/KEY: -35_signal
                    (B) LOCATION:40..45
                    (D) OTHER INFORMATION:/standard_name= "-35 box"

          (ix) FEATURE:
                    (A) NAME/KEY: -10_signal
                    (B) LOCATION:63..68
                    (D) OTHER INFORMATION:/standard_name= "Pribnow box"

          (ix) FEATURE:
                    (A) NAME/KEY: misc_recomb
                    (B) LOCATION:3..25
                    (C) IDENTIFICATION METHOD: experimental
                    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                         /standard_name= "Multiple cloning site"
                         /label= MCS
                         /note= "A sequence specifying recognition sites for the
                         restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
                         MboI, DpnI, AflII, MseI, SspI, NsiI."

          (ix) FEATURE:
                    (A) NAME/KEY: misc_recomb
                    (B) LOCATION:74..98
                    (C) IDENTIFICATION METHOD: experimental
                    (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                         /standard_name= "Multiple cloning site"
                         /label= MCS
                         /note= "A sequence specifying recognition sites for the
                         restriction endonucleases: ScaI, RsaI, HpaI, HincII, MseI,
                         SfcI, PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN NNNNNNNNNT   60

GGTATAATAN NANAGTACTG TTAACTGCAG CTGAATTCGG   100

(2) INFORMATION FOR SEQ ID NO: 2:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 113 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

         (iii) HYPOTHETICAL: YES

          (iv) ANTI-SENSE: NO

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(ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:23..95
        (D) OTHER INFORMATION:/standard_name= "Artificial
            promoter library"
            /note= "A degenerated sequence specifying a mixture of
            artificial temperature regulated promoters covering a wide
            range of expression in small steps in L. lactis"

(ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:23..49
        (D) OTHER INFORMATION:/standard_name= "Sequence providing
            temperature regulation to promoters"
            /note= "This sequence comprising two inverted repeats
            separated by a short spacer provides temperature (heat
            shock) regulation to promoters in Gram-positive bacteria"

(ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:50..60
        (D) OTHER INFORMATION:/standard_name= "Consensus
            sequence"

(ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:75..84
        (D) OTHER INFORMATION:/standard_name= "Consensus
            sequence"

(ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION:89..95
        (D) OTHER INFORMATION:/standard_name= "Consensus
            sequence"

(ix) FEATURE:
        (A) NAME/KEY: -35_signal
        (B) LOCATION:55..60
        (D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:
        (A) NAME/KEY: -10_signal
        (B) LOCATION:78..83
        (D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:
        (A) NAME/KEY: misc_recomb
        (B) LOCATION:3..22
        (D) OTHER INFORMATION:/standard_name= "Multiple cloning
            site"
            /label= MCS
            /note= "A sequence specifying recognition sites for the
            restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
            MboI, DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."

(ix) FEATURE:
        (A) NAME/KEY: misc_recomb
        (B) LOCATION:89..111
        (D) OTHER INFORMATION:/standard_name= "Multiple cloning
            site"
            /label= MCS
            /note= "A sequence specifying recognition sites for the
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restriction endonucleases: ScaI, RsaI, SfcI, PstI, Fnu4HI,
Bbvi, PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGGGATCCAA GCTTAATATT AATTAGCACT CNNNNNNNNN GAGTGCTAAT TTTTTTGACA   60

NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG   113

(2) INFORMATION FOR SEQ ID NO: 3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 199 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: YES

       (iv) ANTI-SENSE: NO

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Saccharomyces cerevisiae

       (ix) FEATURE:
            (A) NAME/KEY: protein_bind
            (B) LOCATION:10..16
            (D) OTHER INFORMATION:/function= "Activating promoters in
                S. cerevisiae"
                /bound_moiety= "GCN4 protein"
                /standard_name= "Upstream activating sequence"
                /label= UAS_GCN4p
                /note= "A DNA sequence that specifies a binding site for
                the GCN4 protein, which activates the transcription of
                genes involved in aminoacid synthesis in S. cerevisiae."

       (ix) FEATURE:
            (A) NAME/KEY: TATA_signal
            (B) LOCATION:67..72
            (D) OTHER INFORMATION:/standard_name= "TATA box"

       (ix) FEATURE:
            (A) NAME/KEY: misc_signal
            (B) LOCATION:122..144
            (D) OTHER INFORMATION:/function= "Transcription
                initiation"
                /standard_name= "TI box"

       (ix) FEATURE:
            (A) NAME/KEY: protein_bind
            (B) LOCATION:122..144
            (D) OTHER INFORMATION:/bound_moiety= "Arginine repressor"
                /standard_name= "arginine repressor binding site"
                /label= argR

       (ix) FEATURE:
            (A) NAME/KEY: misc_RNA
            (B) LOCATION:145..192
            (D) OTHER INFORMATION:/function= "Spacer"
                /standard_name= "Part of native sequence for ARG8

gene incl. first codon"

(ix) FEATURE:
        (A) NAME/KEY: misc_recomb
        (B) LOCATION:3..8
        (D) OTHER INFORMATION:/standard_name= "Recognition site
            for restriction endonuclease EcoRI"
            /label= EcoRI_site

(ix) FEATURE:
        (A) NAME/KEY: misc_recomb
        (B) LOCATION:192..197
        (D) OTHER INFORMATION:/standard_name= "Recognition site
            for restriction endonuclease BamHI"
            /label= BamHI_site

(ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:10..192
        (D) OTHER INFORMATION:/standard_name= "Artificial
            promoter library"
            /note= "A degenerated sequence specifying a mixture of
            artificial promoters covering a wide range of expression
            in small steps in S. cerevisiae"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   60

NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   120

NCTCTTAAGT GCAAGTGACT GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG   180

CTACCAATCA TGGATCCCG   199

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Pseudomonas putida

   (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:1..45
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Artificial promoter library"
            /note= "A degenerated sequence specifying a mixture of
            artificial promoters covering a wide range of expression
            in small steps in Pseudomonas putida"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

NNNNNNNNTT GRNNNNNNNN NNNNNNNNNN NTATRATNNN NNNNN   45

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
           promoter"
           /label= Cp1

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATACCGGAG TTTATTCTTG ACAGTTCCAC CTCGGGTTGA TATAATATCT CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
           promoter"
           /label= Cp10

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..59
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp11

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCCTTTGA TATAATAAGT AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp12

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CATATACAAG TTTATTCTTG ACACTAGTCG GCCAAAATGA TATAATACCT GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid

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            (C)  STRANDEDNESS: double
            (D)  TOPOLOGY: linear

      (ii)  MOLECULE TYPE: DNA (genomic)

     (iii)  HYPOTHETICAL: YES

      (iv)  ANTI-SENSE: NO

       (vi)  ORIGINAL SOURCE:
             (A)  ORGANISM: Lactococcus lactis

      (ix)  FEATURE:
            (A)  NAME/KEY: promoter
            (B)  LOCATION:4..60
            (D)  OTHER INFORMATION:/standard_name= "Constitutional
                  promoter"
                  /label= Cp13

      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CATGCTTTAC TTTATTCTTG ACAAAACCAC CAGCTTTTGG TATAATACGT GAGAACTGTT          60


(2)  INFORMATION FOR SEQ ID NO: 10:

       (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 60 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: double
            (D)  TOPOLOGY: linear

      (ii)  MOLECULE TYPE: DNA (genomic)

     (iii)  HYPOTHETICAL: YES

      (iv)  ANTI-SENSE: NO

       (vi)  ORIGINAL SOURCE:
             (A)  ORGANISM: Lactococcus lactis

      (ix)  FEATURE:
            (A)  NAME/KEY: promoter
            (B)  LOCATION:4..60
            (D)  OTHER INFORMATION:/standard_name= "Constitutional
                  promoter"
                  /label= Cp14

      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA CAGTACTGTT          60


(2)  INFORMATION FOR SEQ ID NO: 11:

       (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 60 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: double
            (D)  TOPOLOGY: linear

      (ii)  MOLECULE TYPE: DNA (genomic)
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   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
         (A) NAME/KEY: promoter
         (B) LOCATION:4..60
         (D) OTHER INFORMATION:/standard_name= "Constitutional
             promoter"
             /label= Cp15

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CATTACNTAG TTNATTCTTG ACAGAATTAC GATTCGCTGG TATAATATAT CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 12:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 58 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

     (iv) ANTI-SENSE: NO

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Lactococcus lactis

     (ix) FEATURE:
          (A) NAME/KEY: promoter
          (B) LOCATION:4..58
          (D) OTHER INFORMATION:/standard_name= "Constitutional
              promoter"
              /label= Cp16

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTTGG TATAATAACA GTACTCAG   58

(2) INFORMATION FOR SEQ ID NO: 13:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 59 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

     (iv) ANTI-SENSE: NO

     (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..59
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..58
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp18

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA GTACTGTT   58

(2) INFORMATION FOR SEQ ID NO: 15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..58

            (D) OTHER INFORMATION:/standard_name= "Constitutional
                promoter"
                /label= Cp19

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATCGCTTAG TTTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA GTACTGTT   58
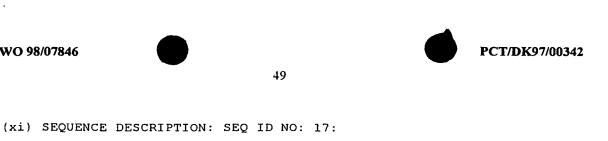

(2) INFORMATION FOR SEQ ID NO: 16:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:4..60
            (D) OTHER INFORMATION:/standard_name= "Constitutional
                promoter"
                /label= Cp2

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CATTTGCTAG TTTATTCTTG ACATGAAGCG TGCCTAATGG TATATTACTT GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 17:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:4..60
            (D) OTHER INFORMATION:/standard_name= "Constitutional
                promoter"
                /label= Cp20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CATGGGTGAG TTTATTCTTG ACAGTGCGGC CNGGGGCTGA TATCATAGCA GAGTACTATT   60

(2) INFORMATION FOR SEQ ID NO: 18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..59
        (D) OTHER INFORMATION:/standard_name= "Constitutional
           promoter"
           /label= Cp21

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CATTACCGAG TTTATTCTTG ACACCGTTTA TCGGGGTTGT ATAATACTAT AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
           promoter"
           /label= Cp23

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp24

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CATGGGTAAG TTTATTCTTC ACACTATCTG GGCCCGATGG TATAATAAGT GACTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

   (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:3..59
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp25

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTTTGGCAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid

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                    (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear

          (ii)  MOLECULE TYPE: DNA (genomic)

         (iii)  HYPOTHETICAL: YES

          (iv)  ANTI-SENSE: NO

          (vi)  ORIGINAL SOURCE:
                    (A)  ORGANISM: Lactococcus lactis

          (ix)  FEATURE:
                    (A)  NAME/KEY: promoter
                    (B)  LOCATION:4..60
                    (D)  OTHER INFORMATION:/standard_name= "Constitutional
                         promoter"
                         /label= Cp26

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CATTCTACAG TTTATTCTTG ACATTGCACT GTCCCCCTGG TATAATAACT ATACATGCAT          60


  (2)  INFORMATION FOR SEQ ID NO: 23:

           (i)  SEQUENCE CHARACTERISTICS:
                    (A)  LENGTH: 60 base pairs
                    (B)  TYPE: nucleic acid
                    (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear

          (ii)  MOLECULE TYPE: DNA (genomic)

         (iii)  HYPOTHETICAL: YES

          (iv)  ANTI-SENSE: NO

          (vi)  ORIGINAL SOURCE:
                    (A)  ORGANISM: Lactococcus lactis

          (ix)  FEATURE:
                    (A)  NAME/KEY: promoter
                    (B)  LOCATION:4..60
                    (D)  OTHER INFORMATION:/standard_name= "Constitutional
                         promoter"
                         /label= Cp28

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CATGGGGCCG TTTATTCTTG ACAACGGCGA GCAGACCTGG TATAATAATA TAGTACTGTT          60


  (2)  INFORMATION FOR SEQ ID NO: 24:

           (i)  SEQUENCE CHARACTERISTICS:
                    (A)  LENGTH: 59 base pairs
                    (B)  TYPE: nucleic acid
                    (C)  STRANDEDNESS: double
                    (D)  TOPOLOGY: linear

          (ii)  MOLECULE TYPE: DNA (genomic)
```

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..59
        (D) OTHER INFORMATION:/standard_name= "Constitutional
           promoter"
           /label= Cp29

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CATCGGTAAG TTATTCTTGA CATCTCAGGG GGGACGTGGT ATAATAACTG AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
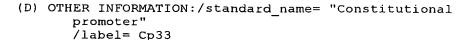   (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
           promoter"
           /label= Cp3

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CATCCTGTAG TTTATTCTTG ACACACGTNN TTAGCTGTGG TATAATAGGA GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:

                    (A) ORGANISM: Lactococcus lactis

          (ix) FEATURE:
                    (A) NAME/KEY: promoter
                    (B) LOCATION:4..60
                    (D) OTHER INFORMATION:/standard_name= "Constitutional
                            promoter"
                            /label= Cp30

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CATGACAGAG TTTATTCTTG ACAGTATTGG GTTACTTTGG TATAATAGTT GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 27:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 60 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (iii) HYPOTHETICAL: YES

          (iv) ANTI-SENSE: NO

          (vi) ORIGINAL SOURCE:
                    (A) ORGANISM: Lactococcus lactis

          (ix) FEATURE:
                    (A) NAME/KEY: promoter
                    (B) LOCATION:4..60
                    (D) OTHER INFORMATION:/standard_name= "Constitutional
                            promoter"
                            /label= Cp32

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CATACGGGAG TTTATTCTTG ACATATTGCC GGTGTGTTGG TATAATAACT TAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 28:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 60 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (iii) HYPOTHETICAL: YES

          (iv) ANTI-SENSE: NO

          (vi) ORIGINAL SOURCE:
                    (A) ORGANISM: Lactococcus lactis

          (ix) FEATURE:
                    (A) NAME/KEY: promoter
                    (B) LOCATION:4..60

        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp33

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CATGTTGGAG TTTATTCTTG ACATACAATT ACTGCAGTGA TATAATAGGT GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 29:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:4..60
            (D) OTHER INFORMATION:/standard_name= "Constitutional
                promoter"
                /label= Cp34

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CATCGCGAAG TTTATTCTTC ACACACCGCA GAACTTGTGG TATAATACAA CAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 30:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 59 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:4..59
            (D) OTHER INFORMATION:/standard_name= "Constitutional
                promoter"
                /label= Cp37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CATCATTAAG TTTATTCTTC ACATTGGCCG GAATTGTTGT ATAATACCTT AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp38

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CATAGAGAAG TTTATTCTTG ACAGCTAACT TGGCCTTTGA TATAATACAT GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp39

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CATTGCGAAG TTTATTCTTG ACAGTACGTT TTTACCATGA TATAATAGTA TAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp4

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GATGTTTTAG TTTATTCTTG ACACCGTATC GTGCGCGTGA TATAATCGGG ATCCTTAAGA   60

(2) INFORMATION FOR SEQ ID NO: 34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp40

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CATAGAACAG TTTATTCTTG ACATTGAATA AGAAGGCTGA TATAATAGCC AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid

```
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

 (iii) HYPOTHETICAL: YES

  (iv) ANTI-SENSE: NO

  (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

  (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp41

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CATCCGCAAG TTTATTCTTG ACAGCTGAAT GTAGACGTGG TATAATAGTT AAGTACTGTT          60


(2) INFORMATION FOR SEQ ID NO: 36:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

 (iii) HYPOTHETICAL: YES

  (iv) ANTI-SENSE: NO

  (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

  (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..60
        (D) OTHER INFORMATION:/standard_name= "Constitutional
            promoter"
            /label= Cp42

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CATTCGTAAG TTTATTCTTG ACACCTGAGA TGAGGCGTGA TATAATAAAT AAGTACTGTT          60


(2) INFORMATION FOR SEQ ID NO: 37:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)
```

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION:4..59
    (D) OTHER INFORMATION:/standard_name= "Constitutional
        promoter"
        /label= Cp44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CATCGGGTAG TTTATTCTTG ACAATTAAGT AGAGCCTGAT ATAATAGTTC AGTACTGTT   59

(2) INFORMATION FOR SEQ ID NO: 38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:4..59
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Constitutional promoter"
            /label= Cp5

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CATGGGGGAG TTTATTCTTG ACATCATCTT CGTAGCCTGG TATACTACAT GAGTATGTT   59

(2) INFORMATION FOR SEQ ID NO: 39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

```
        (vi)  ORIGINAL SOURCE:
              (A)  ORGANISM: Lactococcus lactis

        (ix)  FEATURE:
              (A)  NAME/KEY: promoter
              (B)  LOCATION:4..60
              (D)  OTHER INFORMATION:/standard_name= "Constitutional
                   promoter"
                   /label= Cp6

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CATGTGGGAG TTTATTCTTG ACACAGATAT TTCCGGATGA TATAATAACT GAGTACTGTT        60


(2)  INFORMATION FOR SEQ ID NO: 40:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH: 60 base pairs
             (B)  TYPE: nucleic acid
             (C)  STRANDEDNESS: double
             (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: DNA (genomic)

       (iii)  HYPOTHETICAL: YES

        (iv)  ANTI-SENSE: NO

        (vi)  ORIGINAL SOURCE:
              (A)  ORGANISM: Lactococcus lactis

        (ix)  FEATURE:
              (A)  NAME/KEY: promoter
              (B)  LOCATION:4..60
              (D)  OTHER INFORMATION:/standard_name= "Constitutional
                   promoter"
                   /label= Cp7

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TATGCGGTAG TTTATTCTTG ACATGACGAG ACAGGTGTGG TATAATGGGT CTAGATTAGG        60


(2)  INFORMATION FOR SEQ ID NO: 41:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH: 60 base pairs
             (B)  TYPE: nucleic acid
             (C)  STRANDEDNESS: double
             (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: DNA (genomic)

       (iii)  HYPOTHETICAL: YES

        (iv)  ANTI-SENSE: NO

        (vi)  ORIGINAL SOURCE:
              (A)  ORGANISM: Lactococcus lactis

        (ix)  FEATURE:
              (A)  NAME/KEY: promoter
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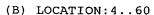
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          (B)  LOCATION:4..60
          (D)  OTHER INFORMATION:/standard_name= "Constitutional
                  promoter"
                  /label= Cp8
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    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CATTCTTTAG TTTATTCTTG ACAAACGTAT TGAGGACTGA TATAATAGGT GAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 42:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 60 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Lactococcus lactis

    (ix) FEATURE:
          (A) NAME/KEY: promoter
          (B) LOCATION:4..60
          (D) OTHER INFORMATION:/standard_name= "Constitutional
                  promoter"
                  /label= Cp9

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CATAGTCTAG TTTATTCTTG ACACGCGGTC CATTGGCTGG TATAATAATT TAGTACTGTT   60

(2) INFORMATION FOR SEQ ID NO: 43:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 177 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
          (A) NAME/KEY: promoter
          (B) LOCATION:8..177
          (C) IDENTIFICATION METHOD: experimental
          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                  /standard_name= "Yeast promoter"
                  /label= Yp102
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG TCCCTCTTAT     60

AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT GCAAGTGACT     120

GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC     177


(2) INFORMATION FOR SEQ ID NO: 44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 182 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION:8..181
        (C) IDENTIFICATION METHOD: experimental
        (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
            /standard_name= "Yeast promoter"
            /label= Yp112

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT GCTGGAGTTC     60

CTTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA GAGGAACCCT     120

CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTTG AATCGCTACC AATCATGGAT     180

CC     182


(2) INFORMATION FOR SEQ ID NO: 45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 191 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:

```
            (A)  NAME/KEY: promoter
            (B)  LOCATION:8..181
            (C)  IDENTIFICATION METHOD: experimental
            (D)  OTHER INFORMATION:/evidence= EXPERIMENTAL
                 /standard_name= "Yeast promoter"
                 /label= Yp13
```

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAATTCGTGA CTCACTAGGC AGGTCACGTT GGCTCTTCGC GGCGCAGGTT CGTATGCCGC   60

GCCGCCAGGG GCTTTATAAA GGTCGTCCTG GGTACAGTTG GGATGGCTCC ACGTTTCGGC   120

TCTTAAGTGC AAGTGACTGC GAACATTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA   180

ATCATGGATC C   191

(2) INFORMATION FOR SEQ ID NO: 46:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 167 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:8..167
            (C) IDENTIFICATION METHOD: experimental
            (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                 /standard_name= "Yeast promoter"
                 /label= Yp15

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG TTTTATAAAT   60

CTTTGGGCCA TGGTCTTGCT GGAAAACACC TCTCTTAAGT GCAAGTGACT GCGAACATTT   120

TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC   167

(2) INFORMATION FOR SEQ ID NO: 47:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 191 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

        (iv) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Saccharomyces cerevisiae

        (ix) FEATURE:
             (A) NAME/KEY: promoter
             (B) LOCATION:8..191
             (C) IDENTIFICATION METHOD: experimental
             (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                    /standard_name= "Yeast promoter"
                    /label= Yp154

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG GGGCGTTCTA   60

GCGCAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTTGTCT AGTTTGACTC   120

TTAAGTGCAA GTGACTGCGA ACATTTTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA   180

ATCATGGATC C   191

(2) INFORMATION FOR SEQ ID NO: 48:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 195 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

        (iii) HYPOTHETICAL: YES

        (iv) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Saccharomyces cerevisiae

        (ix) FEATURE:
             (A) NAME/KEY: promoter
             (B) LOCATION:8..190
             (C) IDENTIFICATION METHOD: experimental
             (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                    /standard_name= "Yeast promoter"
                    /label= Yp18

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GAATTCGTGA CTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG GAGGTGAGAA   60

GCTTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTTGGT GGGATAGGGG GTACTGTACC   120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT   180

ACCAATCATG GATCC   195

(2) INFORMATION FOR SEQ ID NO: 49:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 179 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
          (A) NAME/KEY: promoter
          (B) LOCATION:8..179
          (C) IDENTIFICATION METHOD: experimental
          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
             /standard_name= "Yeast promoter"
             /label= Yp183

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GAATTCGTGA CTCACTAAGG GTTCGCCATT AACAGAATCG CTGGTAGAAC ATCGGTAGTT   60

AGGCACCCGA GTATAAACAG GCGGACCCCT CACGGATATC AGCTGATAGT GCGAGCCTCA   120

ATGCGAACAT TTTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT CATGGATCC   179

(2) INFORMATION FOR SEQ ID NO: 50:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 195 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: YES

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Saccharomyces cerevisiae

    (ix) FEATURE:
          (A) NAME/KEY: promoter
          (B) LOCATION:8..190
          (C) IDENTIFICATION METHOD: experimental
          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
             /standard_name= "Yest promoter"
             /label= Yp190

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GAATTCGTGA CTCAGTATCC ACGGGTGTTT GAGGGCTGGT CGCAGGTTAG CAGGCGAGGG   60

CGGGTGGTTA CGGCTATAAA TGAGTGTTTG CAGCCGGGTA CGGGCGTACG AGTAGTGATC   120

TCTTAAATGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT   180

ACCAATCATG GATCC   195

    (2) INFORMATION FOR SEQ ID NO: 51:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 193 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: YES

       (iv) ANTI-SENSE: NO

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Saccharomyces cerevisiae

       (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:8..189
            (C) IDENTIFICATION METHOD: experimental
            (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                /standard_name= "Yest promoter"
                /label= Yp191

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAATTCGTGA CTCAATGCTG CGGGCGGCAG GAGTCTGGTG TAACTTCCCA TTTTGAGTGA   60

AAGACAGACC ATCTATAAAC ATTTGGTGGG CAAAGTGGCC TGGCGGATTT GTTTGGACTC   120

TTAAGTGAAA GTGACTGCGA ACATTTTTTT CGTTTGTTAG AATAATTCAA GAATCGCTAC   180

CAATCATGGA TCC   193

(2) INFORMATION FOR SEQ ID NO: 52:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 166 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: YES

       (iv) ANTI-SENSE: NO

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Saccharomyces cerevisiae

       (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:8..166
            (C) IDENTIFICATION METHOD: experimental
            (D) OTHER INFORMATION:/evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"
/label= Yp192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GAATTCGTGA CTCACTTAAG GCTACTGCGG AAGTTTAGAT CTAAGGTCGG AAATAATTTA   60

GAAAATTACG ACATTATAAA TAGCGGAGAG GCCAGGTGAT GGGCACCATT GTGGGGGGGC   120

TCTTAATTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC   166

(2) INFORMATION FOR SEQ ID NO: 53:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 195 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: YES

        (iv) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Saccharomyces cerevisiae

        (ix) FEATURE:
            (A) NAME/KEY: promoter
            (B) LOCATION:8..190
            (C) IDENTIFICATION METHOD: experimental
            (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                /standard_name= "Yeast promoter"
                /label= Yp212

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAATTCGTGA CTCAGTCGCC CGCAAGATGG GATGGTGCAT TTTAAACACC CGAATTATAC   60

TCGTCAACTT ATAGTATAAA CGGAACGCGA CGATACGTTC TAGTTTTCGG CGAAGTCGAC   120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT   180

ACCAATCATG GATCC   195

(2) INFORMATION FOR SEQ ID NO: 54:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 188 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: YES

        (iv) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:

```
                  (A) ORGANISM: Saccharomyces cerevisiae

          (ix) FEATURE:
                  (A) NAME/KEY: promoter
                  (B) LOCATION:8..183
                  (C) IDENTIFICATION METHOD: experimental
                  (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                      /standard_name= "Yeast promoter"
                      /label= Yp24

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATTCGTAC TCACGACAGC GTTATGACTT CGAGGACCAG CTACTTCCGG TCGCGTACTA        60

GTTTTTACCT GTATAAACTT TGCTACCGCT GGGCCTTGGT GGTGCTGTCC CGCTCTTAAG       120

TGCAAGTGAC TGCGAACATT TTTTTCGTTT GTTACAATAA TTCAAGAATC GCTACCAATC       180

ATGGATCC                                                              188
```

(2) INFORMATION FOR SEQ ID NO: 55:

```
          (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 195 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (iii) HYPOTHETICAL: YES

          (iv) ANTI-SENSE: NO

          (vi) ORIGINAL SOURCE:
                  (A) ORGANISM: Saccharomyces cerevisiae

          (ix) FEATURE:
                  (A) NAME/KEY: promoter
                  (B) LOCATION:8..190
                  (C) IDENTIFICATION METHOD: experimental
                  (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
                      /standard_name= "Yeast promoter"
                      /label= Yp435

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GAATTCGTGA CTAAATGGAT AAGGTTATCG CCATCACGGA GTCTTCTCTC ACGTCTGGAG        60

CAGAGGCTAG ACCTTATAAA TTATACATGG TGGGAGAGGC GATAGTCTTT AGAGACGTGC       120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT       180

ACCAATCATG GATCC                                                       195
```

(2) INFORMATION FOR SEQ ID NO: 56:

```
          (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 189 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
```

```
          (D)  TOPOLOGY: linear

     (ii)  MOLECULE TYPE: DNA (genomic)

    (iii)  HYPOTHETICAL: YES

     (iv)  ANTI-SENSE: NO

     (vi)  ORIGINAL SOURCE:
           (A)  ORGANISM: Saccharomyces cerevisiae

     (ix)  FEATURE:
           (A)  NAME/KEY: promoter
           (B)  LOCATION:8..184
           (C)  IDENTIFICATION METHOD: experimental
           (D)  OTHER INFORMATION:/evidence= EXPERIMENTAL
                  /standard_name= "Yeast promoter"
                  /label= Yp68

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 56:
```

GAATTCGTGA CTCACAAGAA TGTGGGCGGG TCGTTAAACT GAGCCTGGAC ACCTTGGCTG   60

CGTCGCTTTC GTATAAAGAT CTTAGAGCTG TGGAGTCTGG GTCGAGTGGC CAGCTCTTAA   120

ATGCAAGTGA CTGCGAACAT TTTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT   180

CATGGATCC   189


```
(2)  INFORMATION FOR SEQ ID NO: 57:

      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 195 base pairs
           (B)  TYPE: nucleic acid
           (C)  STRANDEDNESS: double
           (D)  TOPOLOGY: linear

     (ii)  MOLECULE TYPE: DNA (genomic)

    (iii)  HYPOTHETICAL: YES

     (iv)  ANTI-SENSE: NO

     (vi)  ORIGINAL SOURCE:
           (A)  ORGANISM: Saccharomyces cerevisiae

     (ix)  FEATURE:
           (A)  NAME/KEY: promoter
           (B)  LOCATION:8..190
           (C)  IDENTIFICATION METHOD: experimental
           (D)  OTHER INFORMATION:/evidence= EXPERIMENTAL
                  /standard_name= "Yeast promoter"
                  /label= Yp89

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 57:
```

GAATTCGTGA CTCACTCGGA AGATTGGGTT TACGATTAGG ATGGCGCGGC AGAACCGGGG   60

GGGATTCCCT TCTATATAAA GGGTTCCGAT ACTACGTGCT GCGGACGGCC GATCGAGTTA   120

TCTTAAGTGC AAGTGACTGC GAAAATTTTT TTCGTTTGTT AGAATAATTC ΛAAGAATCGCT   180

ACCAATCATG GATCC 195

(2) INFORMATION FOR SEQ ID NO: 58:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 176 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: YES

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Saccharomyces cerevisiae

   (ix) FEATURE:
       (A) NAME/KEY: promoter
       (B) LOCATION:8..171
       (C) IDENTIFICATION METHOD: experimental
       (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
           /standard_name= "Yeast promoter"
           /label= Yp96

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAATTCGTGA CTCATCTAGT GAGAGGAGCC GTGGTATCTT GTGTCACCAC CAGGGGAAAA   60

TAATGGCAGG GGTGTATAAA TGGTCGAGTA GTCGCGACCC ACGCTGCAAG GCAAGGAACT   120

CTTAAATTTT TTTCGTTTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC   176